

AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

1. (Currently amended) Method for detecting ~~analyzing~~ the presence of a bacterial pathogen in a clinical sample comprising the steps of:

at least partially isolating nucleic acid from said sample, ~~characterized in that wherein~~ said nucleic acid is selected from a group consisting of either total nucleic acid, total DNA ~~or~~ and total RNA,

quantifying the an amount of nucleic acid from said sample comprising a ~~preselected~~ sequence the 16S/23S rDNA spacer region which is specific for said bacterial pathogen; ~~wherein said step of quantifying the amount of said nucleic acid is performed by means of amplification- Polymerase Chain Reaction which is monitored in real time by means of a hybridization probe,~~

further comprising ~~the step of~~ monitoring temperature dependence of hybridization, and

determining whether said amount of nucleic acid from said sample comprising a ~~preselected sequence the 16S/23S rDNA spacer region which is specific for said bacterial pathogen-exceeds~~ is above a first predetermined cut off value, is less than a second predetermined cut off value which is less than said first predetermined cut off value, or is less than said first predetermined cut off value and above said second predetermined cut off value,

wherein said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is indicative of the presence of said bacterial pathogen if said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region exceeds is above said first predetermined cut off value,

wherein said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is indicative of the absence of said bacterial pathogen if said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is less than said second predetermined cut off value, or

wherein said bacterial pathogen is not confirmed nor excluded if said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is above said second predetermined cut off value but is less than said first predetermined cut off value; and

wherein said monitoring temperature dependence of hybridization is indicative of indicates
the presence of a group of predetermined species of said bacterial pathogen.

2. (Canceled).
3. (Canceled).
4. (Canceled).
5. (Previously amended) Method according to claim 1,
wherein said clinical sample is whole blood.
6. (Previously amended) Method according to claim 1,
wherein said bacterial pathogen is selected from a group consisting of Coagulase negative
Staphylococci and Enterococci.
7. (Canceled).
8. (Canceled).